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<p>(54) Title: HUMAN PROTEASE AND USE OF SUCH PROTEASE FOR PHARMACEUTICAL APPLICATIONS AND FOR REDUCING THE ALLERGENICITY OF NON-HUMAN PROTEINS</p> <p>(57) Abstract</p> <p>The present invention relates to a method of producing novel improved protein mutant which produce low allergenic response in humans compared to the parent of that mutant. Specifically, the present invention comprises neutralizing or reducing the allergenicity of a protein by introducing therein as replacement or modification of an epitope on such protein a sequence from human subtilisin.</p>			

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HUMAN PROTEASE AND USE OF SUCH PROTEASE FOR PHARMACEUTICAL APPLICATIONS AND FOR REDUCING THE ALLERGENICITY OF NON-HUMAN PROTEINS

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BACKGROUND OF THE INVENTION

A. Field of the Invention

The present invention relates to a human protein sequence which can be used in several applications. Specifically, the novel human protein sequence can be used to design proteins which produce lower allergenic response in humans exposed to such proteins through the use of a predictive assay.

B. State of the Art

15 Serine proteases are a subgroup of carbonyl hydrolases. They comprise a diverse class of enzymes having a wide range of specificities and biological functions. Stroud, R. Sci. Amer., 131:74-88. Despite their functional diversity, the catalytic machinery of serine proteases has been approached by at least two genetically distinct families of enzymes: the subtilisins and the mammalian chymotrypsin related and homologous bacterial serine proteases (e.g., trypsin and *S. gresius* trypsin). These two families of serine proteases show remarkably similar mechanisms of catalysis. Kraut, J. (1977), Ann. Rev. Biochem., 46:331-358. Furthermore, although the primary structure is unrelated, the tertiary structure of these two enzyme families bring together a conserved catalytic triad of amino acids consisting of serine, histidine and aspartate.

25 Subtilisin is a serine endoprotease (MW 27,500) which is secreted in large amounts from a wide variety of *Bacillus* species and other microorganisms. The protein sequence of subtilisin has been determined from at least four different species of *Bacillus*. Markland, F.S., et al. (1983), Honne-Seyler's Z. Physiol. Chem., 364:1537-1540. The three-dimensional crystallographic structure of *Bacillus amyloliquefaciens* subtilisin to 2.5A
30 resolution has also been reported. Wright, C.S., et al. (1969), Nature, 221:235-242; Drenth, J., et al. (1972), Eur. J. Biochem., 26:177-181. These studies indicate that although subtilisin is genetically unrelated to the mammalian chymotrypsin like serine proteases, it has a similar active site structure. The x-ray crystal structures of subtilisin containing covalently bound peptide inhibitors (Robertus, J.D., et al. (1972), Biochemistry, 35 11:2439-2449) or product complexes (Robertus, J.D., et al. (1976), J. Biol. Chem., 251:1097-1103) have also provided information regarding the active site and putative substrate binding cleft of subtilisin. In addition, a large number of kinetic and chemical

modification studies have been reported for subtilisin (Philipp, M., et al. (1983), Mol. Cell. Biochem., 51:5-32; Svendsen, B. (1976), Carlsberg Res. Comm., 41:237-291; Markland, F.S. Id.) as well as at least one report wherein the side chain of methionine at residue 222 of subtilisin was converted by hydrogen peroxide to methionine-sulfoxide (Stauffer, D.C., 5 et al. (1965), J. Biol. Chem., 244:5333-5338) and the side chain of serine at residue 221 converted to cysteine by chemical modification (Polgar, et al. (1981), Biochimica et Biophysica Acta, 667:351-354.)

10 Proteins bearing some resemblance and/or homology to bacterial subtilisin have also been detected in humans as well (see e.g., Keifer et al., DNA and Cell Biol., Vol. 10, No. 10, pp. 757-769 (1991); Smeekens et al., J. Biol. Chem., Vol. 265, No. 6, pp. 2997-3000 (1990); Tomkinson et al., Biochem., Vol. 30, pp. 168-174 (1991)).

15 US Patent 4,760,025 (RE 34,606) discloses the modification of subtilisin amino acid residues corresponding to positions in *Bacillus amyloliquefaciens* subtilisin tyrosine -1, aspartate +32, asparagine +155, tyrosine +104, methionine +222, glycine +166, histidine +64, glycine +169, phenylalanine +189, serine +33, serine +221, tyrosine +217, glutamate +156 and alanine +152. US Patent 5,182,204 discloses the modification of the amino acid +224 residue in *Bacillus amyloliquefaciens* subtilisin and equivalent positions in other subtilisins which may be modified by way of substitution, insertion or deletion and which may be combined with modifications to the residues identified in US Patent 20 4,760,025 (RE 34,606) to form useful subtilisin mutants or variants. US Patent 5,155,033 discloses similar mutant subtilisins having a modification at an equivalent position to +225 of *B. amyloliquefaciens* subtilisin. US Patents 5,185,258 and 5,204,015 disclose mutant subtilisins having a modification at positions +123 and/or +274. US Patent 5,182,204 discloses the modification of many amino acid residues within subtilisin, including 25 specifically +99, +101, +103, +107, +126, +128, +135, +197 and +204. US Patent 4,914,031 discloses certain subtilisin analogs, including a subtilisin modified at position +76.

30 Proteins, including proteases, used in industrial, pharmaceutical and commercial applications are of increasing prevalence. As a result, the increased exposure due to this prevalence has been responsible for some safety hazards caused by the sensitization of certain persons to those peptides, whereupon subsequent exposure causes extreme allergic reactions which can be injurious and even fatal. For example, proteases are known to cause dangerous hypersensitivity in some individuals. As a result, despite the usefulness of proteases in industry, e.g., in laundry detergents, cosmetics, textile 35 treatment etc...., and the extensive research performed in the field to provide improved

proteases which have, for example, more effective stain removal under detergency conditions, the use of proteases in industry has been problematic due to their ability to produce a hypersensitive allergic response in some humans.

Much work has been done to alleviate these problems. Among the strategies 5 explored to reduce immunogenic potential of protease use have been improved production processes which reduce potential contact by controlling and minimizing workplace concentrations of dust particles or aerosol carrying airborne protease, improved granulation processes which reduce the amount of dust or aerosol actually produced from the protease product, and improved recovery processes to reduce the level of potentially 10 allergenic contaminants in the final product. However, efforts to reduce the allergenicity of protease, per se, have been relatively unsuccessful. Alternatively, efforts have been made to mask epitopes in protease which are recognized by immunoglobulin E (IgE) in hypersensitive individuals (PCT Publication No. WO 92/10755) or to enlarge or change the 15 nature of the antigenic determinants by attaching polymers or peptides/proteins to the problematic protease.

When an adaptive immune response occurs in an exaggerated or inappropriate form, the individual experiencing the reaction is said to be hypersensitive. Hypersensitivity reactions are the result of normally beneficial immune responses acting inappropriately and sometimes cause inflammatory reactions and tissue damage. They can be provoked 20 by many antigens; and the cause of a hypersensitivity reaction will vary from one individual to the next. Hypersensitivity does not normally manifest itself upon first contact with the antigen, but usually appears upon subsequent contact. One form of hypersensitivity occurs when an IgE response is directed against innocuous environmental 25 antigens, such as pollen, dust-mites or animal dander. The resulting release of pharmacological mediators by IgE-sensitized mast cells produces an acute inflammatory reaction with symptoms such as asthma or rhinitis.

Nonetheless, a strategy comprising modifying the IgE sites will not generally be successful in preventing the cause of the initial sensitization reaction. Accordingly, such 30 strategies, while perhaps neutralizing or reducing the severity of the subsequent hypersensitivity reaction, will not reduce the number of persons actually sensitized. For example, when a person is known to be hypersensitive to a certain antigen, the general, and only safe, manner of dealing with such a situation is to isolate the hypersensitive person from the antigen as completely as possible. Indeed, any other course of action 35 would be dangerous to the health of the hypersensitive individual. Thus, while reducing

the danger of a specific protein for a hypersensitive individual is important, for industrial purposes it would be far more valuable to render a protein incapable of initiating the hypersensitivity reaction in the first place.

5 T-lymphocytes (T-cells) are key players in the induction and regulation of immune responses and in the execution of immunological effector functions. Specific immunity against infectious agents and tumors is known to be dependent on these cells and they are believed to contribute to the healing of injuries. On the other hand, failure to control these responses can lead to auto aggression. In general, antigen is presented to T-cells

10 in the form of antigen presenting cells which, through a variety of cell surface mechanisms, capture and display antigen or partial antigen in a manner suitable for antigen recognition by the T-cell. Upon recognition of a specific epitope by the receptors on the surface of the T-cells (T-cell receptors), the T-cells begin a series of complex interactions, including proliferation, which result in the production of antibody by B-cells.

15 While T-cells and B-cells are both activated by antigenic epitopes which exist on a given protein or peptide, the actual epitopes recognized by these mononuclear cells are generally not identical. In fact, the epitope which activates a T-cell to initiate the creation of immunologic diversity is quite often not the same epitope which is later recognized by B-cells in the course of the immunologic response. Thus, with respect to hypersensitivity,

20 while the specific antigenic interaction between the T-cell and the antigen is a critical element in the initiation of the immune response to antigenic exposure, the specifics of that interaction, i.e., the epitope recognized, is often not relevant to subsequent development of a full blown allergic reaction.

25 PCT Publication No. WO 96/40791 discloses a process for producing polyalkylene oxide-polypeptide conjugates with reduced allergenicity using polyalkylene oxide as a starting material.

30 PCT Publication No. WO 97/30148 discloses a polypeptide conjugate with reduced allergenicity which comprises one polymeric carrier molecule having two or more polypeptide molecules coupled covalently thereto.

35 PCT Publication No. WO 96/17929 discloses a process for producing polypeptides with reduced allergenicity comprising the step of conjugating from 1 to 30 polymolecules to a parent polypeptide.

40 PCT Publication No. WO 92/10755 discloses a method of producing protein variants evoking a reduced immunogenic response in animals. In this application, the proteins of interest, a series of proteases and variants thereof, were used to immunized

rats. The sera from the rats was then used to measure the reactivity of the polyclonal antibodies already produced and present in the immunized sera to the protein of interest and variants thereof. From these results, it was possible to determine whether the antibodies in the preparation were comparatively more or less reactive with the protein and its variants, thus permitting an analysis of which changes in the protein are likely to neutralize or reduce the ability of the Ig to bind. From these tests on rats, the conclusion was arrived at that changing any of subtilisin 309 residues corresponding to 127, 128, 129, 130, 131, 151, 136, 151, 152, 153, 154, 161, 162, 163, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 186, 193, 194, 195, 196, 197, 247, 251, 261 will result in a change in the immunological potential.

PCT Publication No. WO 94/10191 discloses low allergenic proteins comprising oligomeric forms of the parent monomeric protein, wherein the oligomer has substantially retained its activity.

The prior art has provided methods of reducing the allergenicity of certain proteins and identification of epitopes which cause allergic reactions in some individuals, the assays used to identify these epitopes generally involving measurement of IgE and IgG antibody in blood sera previously exposed to the antigen. Nonetheless, a need continues for alternate methods of preparing low allergenicity enzymes. Likewise, a need exists for an increased availability of human enzymes which may have use in pharmaceutical applications.

SUMMARY OF THE INVENTION

It is an object of the invention to provide a human protease which can be used in industry as a replacement for bacterial and fungal proteases.

It is an object of the invention to provide a method of making currently used and successful proteases and other proteins more safe by integrating therein sequences derived from human protease analogs.

It is a further object of the invention to provide a human protease which may have application in the pharmaceutical industry.

According to the present invention, a method for reducing the allergenicity of a non-human protein is provided wherein an epitope is identified and replaced with an analogous region within a human subtilisin. In a preferred embodiment the non-human protein is an enzyme, more preferably a protease. In another preferred embodiment, the epitope replaced is a T-cell epitope.

In another embodiment of the present invention, a method for producing the protein of the invention having reduced allergenicity is provided. Preferably, the mutant protein is prepared by modifying a DNA encoding a precursor protein so that the modified DNA encodes the mutant protein of the invention wherein an epitope is replaced with an analogous region from human subtilisin.

In yet another embodiment of the invention, DNA sequences encoding the mutant protein, as well as expression vectors containing such DNA sequences and host cells transformed with such vectors are provided, which host cells are preferably capable of expressing such DNA to produce the mutant protein of the invention either intracellularly or extracellularly.

The mutant protein of the invention is useful in any composition or process in which the protein is generally known to be useful. For example, where the protein is a protease, the reduced allergenicity protease can be used as a component in cleaning products such as laundry detergents and hard surface cleansers, as an aid in the preparation of leather, in the treatment of textiles such as wool and/or silk to reduce felting, as a component in a cosmetic or face cream, and as a component in animal or pet feed to improve the nutritional value of the feed. Similarly, where the protein is an amylase, the reduced allergenicity amylase can be used for the liquefaction of starch, as a component in a dishwashing detergent, for desizing of textiles, in a laundry detergent or any other use for which amylase is useful. Similarly, where the protein is a pharmaceutical composition, its use can be made more safe by reducing the possibility of allergic reaction.

In another embodiment of the invention, the human subtilisin may be used in pharmaceutical applications wherein the protease is used for debridement treatments.

25

BRIEF DESCRIPTION OF THE DRAWINGS

Figs. 1 A-C illustrates the DNA (SEQ ID:NO 1) and amino acid (SEQ ID:NO 2) sequence for *Bacillus amyloliquefaciens* subtilisin (BPN') and a partial restriction map of this gene.

30 Fig. 2 illustrates the conserved amino acid residues among subtilisins from *Bacillus amyloliquefaciens* and *Bacillus lentinus* (wild-type)(SEQ ID:NO 3).

35 Figs. 3A and 3B illustrate an amino acid sequence alignment of subtilisin type proteases from *Bacillus amyloliquefaciens* (BPN'), *Bacillus subtilis*, *Bacillus licheniformis* (SEQ ID:NO 4) and *Bacillus lentinus*. The symbol * denotes the absence of specific amino acid residues as compared to subtilisin BPN'.

Fig. 4. illustrates the additive T-cell response of 16 peripheral mononuclear blood samples to peptides corresponding to the *Bacillus lenthus* protease. Peptide E05 represents the region comprising residues corresponding to 170-173 in protease from *Bacillus amyloliquefaciens*.

5 Fig. 5 illustrate the additive T-cell response of 10 peripheral mononuclear blood sample to peptides corresponding to the human subtilisin.

Fig. 6 illustrates the amino acid sequence of human subtilisin (SEQ ID: NO 6).

Fig. 7 illustrates the amino acid strings corresponding to peptides derived from the sequence of *Bacillus lenthus* protease used in Example 2.

10 Figs. 8A and 8B illustrate the amino acid strings corresponding to peptides derived from the sequence of human subtilisin used in Example 2.

DETAILED DESCRIPTION OF THE INVENTION

According to the present invention, a method for reducing the allergenicity of a 15 non-human protein is provided wherein an epitope is identified and replaced with an analogous region within a human subtilisin. In a preferred embodiment the non-human protein is an enzyme, more preferably a protease. In another preferred embodiment, the epitope replaced is a T-cell epitope.

In another embodiment of the present invention, a method for producing the 20 protein of the invention having reduced allergenicity is provided. Preferably, the mutant protein is prepared by modifying a DNA encoding a precursor protein so that the modified DNA encodes the mutant protein of the invention wherein an epitope is replaced with an analogous region from human subtilisin.

In yet another embodiment of the invention, DNA sequences encoding the mutant 25 protein, as well as expression vectors containing such DNA sequences and host cells transformed with such vectors are provided, which host cells are preferably capable of expressing such DNA to produce the mutant protein of the invention either intracellularly or extracellularly.

According to a preferred embodiment of the present invention, the epitope to be 30 replaced in the non-human protein of interest is identified by a method for identifying T-cell epitopes. In a preferred embodiment of the invention, the present invention provides an assay which identifies epitopes as follows: differentiated dendritic cells are combined with naïve human CD4+ and/or CD8+ T-cells and with a peptide of interest. More specifically, a method is provided wherein a T-cell epitope is recognized comprising the steps of: (a) 35 obtaining from a single blood source a solution of dendritic cells and a solution of naïve

CD4+ and/or CD8+ T-cells; (b) promoting differentiation in said solution of dendritic cells; (c) combining said solution of differentiated dendritic cells and said naïve CD4+ and/or CD8+ T-cells with a peptide of interest; (d) measuring the proliferation of T-cells in said step (c).

5 The non-human peptide of interest to be analyzed according to the assay of the invention is derived from a protein or enzyme for which reduced allergenicity is required. In the practice of the invention, it is possible to identify with precision the location of an epitope which can cause sensitization in an individual or sampling of individuals. In a particularly effective embodiment of the invention, a series of peptide oligomers which 10 correspond to all or part of the protein or enzyme are prepared. For example, a peptide library is produced covering the relevant portion or all of the protein. One particularly useful manner of producing the peptides is to introduce overlap into the peptide library, for example, producing a first peptide corresponds to amino acid sequence 1-10 of the subject protein, a second peptide corresponds to amino acid sequence 4-14 of the subject 15 protein, a third peptide corresponds to amino acid sequence 7-17 of the subject protein, a fourth peptide corresponds to amino acid sequence 10-20 of the subject protein etc. . . until representative peptides corresponding to the entire molecule are created. By analyzing each of the peptides individually in the assay provided herein, it is possible to precisely identify the location of epitopes recognized by T-cells. In the example above, the 20 reaction of one specific peptide to a greater extent than its neighbors will facilitate identification of the epitope anchor region to within three amino acids. After determining the location of these epitopes, it is possible to alter the amino acids within each epitope until the peptide produces a less significant T-cell response.

Preferably, the epitope is modified in one of the following ways: (a) preferably the 25 amino acid sequence of the epitope is substituted with an analogous sequence from the human subtilisin of the invention to the protein of interest, e.g., where the protein is a subtilisin, a sequence alignment can be arranged so as to find the analogous region in the human subtilisin molecule with which to replace the pertinent epitope in the subtilisin; (b) the amino acid sequence of the epitope is substituted with a sequence from human 30 subtilisin of the invention which substantially mimics the major tertiary structure attributes of the epitope, but which produces a lesser allergenic response due to T-cell epitope recognition than that of the protein of interest; or (c) with any sequence from the human subtilisin of the invention which produces lesser allergenic response due to T-cell epitope recognition than that of the protein of interest.

"Antigen presenting cell" as used herein means a cell of the immune system which present antigen on their surface which is recognizable by T-cells. Examples of antigen presenting cells are dendritic cells, interdigitating cells, activated B-cells and macrophages.

5 "T-cell proliferation" as used herein means the number of T-cells produced during the incubation of T-cells with the antigen presenting cells, with or without antigen.

"Baseline T-cell proliferation" as used herein means T-cell proliferation which is normally seen in an individual in response to exposure to antigen presenting cells in the absence of peptide or protein antigen. For the purposes herein, the baseline T-cell 10 proliferation level was determined on a per sample basis for each individual as the proliferation of T-cells in response to antigen presenting cells in the absence of antigen.

"T-cell epitope" means a feature of a peptide or protein which is recognized by a T-cell receptor in the initiation of an immunologic response to the peptide comprising that antigen. Recognition of a T-cell epitope by a T-cell is generally believed to be via a 15 mechanism wherein T-cells recognize peptide fragments of antigens which are bound to class I or class II major histocompatibility (MHC) molecules expressed on antigen-presenting cells (see e.g., Moeller, G. ed., Antigenic Requirements for Activation of MHC-Restricted Responses, Immunological Review, Volume 98, p 187 (Copenhagen; Munksgaard) (1987).

20 The epitopes determined according to the assay provided herein are then modified to reduce the allergenic potential of the protein of interest. In a preferred embodiment, the epitope to be modified produces a level of T-cell proliferation of greater than three times the baseline T-cell proliferation in a sample. When modified, the epitope produces less than three times the baseline proliferation, preferably less than two times the baseline 25 proliferation and most preferably less than or substantially equal to the baseline proliferation in a sample.

"Sample" as used herein comprises mononuclear cells which are naïve, i.e., not sensitized, to the antigen in question.

30 "Homolog" as used herein means a protein or enzyme which has similar catalytic action, structure and/or use as the protein of interest. It is desirable to find a homolog that has a tertiary and/or primary structure similar to the protein of interest as replacement of the epitope in the protein of interest with an analogous segment from the homolog will reduce the disruptiveness of the change. Thus, enzymes having significant homology will provide the most desirable target for epitope substitutions with sequences from the human 35 subtilisin of the invention.

An "analogous" sequence may be determined by ensuring that the replacement amino acids show a similar function, the tertiary structure and/or conserved residues to the amino acids in the protein of interest at or near the epitope. Thus, where the epitope region contains, for example, an alpha-helix or a beta-sheet structure, the replacement amino acids should maintain that specific structure.

While the present invention extends to all proteins for which it is desired to reduce allergenicity, for the sake of simplicity, the following will describe a particularly preferred embodiment of the invention, the modification of protease. Proteases are carbonyl hydrolases which generally act to cleave peptide bonds of proteins or peptides. As used herein, "protease" means a naturally-occurring protease or a recombinant protease. Naturally-occurring proteases include α -aminoacylpeptide hydrolase, peptidylamino acid hydrolase, acylamino hydrolase, serine carboxypeptidase, metallocarboxypeptidase, thiol proteinase, carboxylproteinase and metalloproteinase. Serine, metallo, thiol and acid proteases are included, as well as endo and exo-proteases.

Subtilisins are bacterial or fungal proteases which generally act to cleave peptide bonds of proteins or peptides. As used herein, "subtilisin" means a naturally-occurring subtilisin or a recombinant subtilisin. A series of naturally-occurring subtilisins is known to be produced and often secreted by various microbial species. Amino acid sequences of the members of this series are not entirely homologous. However, the subtilisins in this series exhibit the same or similar type of proteolytic activity. This class of serine proteases shares a common amino acid sequence defining a catalytic triad which distinguishes them from the chymotrypsin related class of serine proteases. The subtilisins and chymotrypsin related serine proteases both have a catalytic triad comprising aspartate, histidine and serine. In the subtilisin related proteases the relative order of these amino acids, reading from the amino to carboxy terminus, is aspartate-histidine-serine. In the chymotrypsin related proteases, the relative order, however, is histidine-aspartate-serine. Thus, subtilisin herein refers to a serine protease having the catalytic triad of subtilisin related proteases. Examples include but are not limited to the subtilisins identified in Fig. 3 herein. Generally and for purposes of the present invention, numbering of the amino acids in proteases corresponds to the numbers assigned to the mature *Bacillus amyloliquefaciens* subtilisin sequence presented in Fig. 1.

"Recombinant subtilisin" or "recombinant protease" refer to a subtilisin or protease in which the DNA sequence encoding the subtilisin or protease is modified to produce a variant (or mutant) DNA sequence which encodes the substitution, deletion or insertion of

on or more amino acids in the naturally-occurring amino acid sequence. Suitable methods to produce such modification, and which may be combined with those disclosed herein, include those disclosed in US Patent 4,760,025 (RE 34,606), US Patent 5,204,015 and US Patent 5,185,258.

5 "Non-human subtilisins" and the DNA encoding them may be obtained from many procaryotic and eucaryotic organisms. Suitable examples of procaryotic organisms include gram negative organisms such as *E. coli* or *Pseudomonas* and gram positive bacteria such as *Micrococcus* or *Bacillus*. Examples of eucaryotic organisms from which subtilisin and their genes may be obtained include yeast such as *Saccharomyces cerevisiae*, fungi such as *Aspergillus* sp.

10 "Human subtilisin" means the protein represented by the sequence in Fig. 6, derivatives thereof or modifications thereof which retain the essential ability to hydrolyze peptide bonds.

15 A "protease variant" has an amino acid sequence which is derived from the amino acid sequence of a "precursor protease". The precursor proteases include naturally-occurring proteases and recombinant proteases. The amino acid sequence of the protease variant is "derived" from the precursor protease amino acid sequence by the substitution, deletion or insertion of one or more amino acids of the precursor amino acid sequence. Such modification is of the "precursor DNA sequence" which encodes the 20 amino acid sequence of the precursor protease rather than manipulation of the precursor protease enzyme *per se*. Suitable methods for such manipulation of the precursor DNA sequence include methods disclosed herein, as well as methods known to those skilled in the art (see, for example, EP 0 328299, WO89/06279 and the US patents and applications already referenced herein).

25 These amino acid position numbers used herein refer to those assigned to the mature *Bacillus amyloliquefaciens* subtilisin sequence presented in Fig. 1. The invention, however, is not limited to the mutation of this particular subtilisin but extends to precursor proteases containing amino acid residues at positions which are "equivalent" to the particular identified residues in *Bacillus amyloliquefaciens* subtilisin. In a preferred 30 embodiment of the present invention, the precursor protease is *Bacillus lenthus* subtilisin and the substitutions, deletions or insertions are made at the equivalent amino acid residue in *B. lenthus* corresponding to those listed above.

35 A residue (amino acid) of a precursor protease is equivalent to a residue of *Bacillus amyloliquefaciens* subtilisin if it is either homologous (i.e., corresponding in

position in either primary or tertiary structure) or analogous to a specific residue or portion of that residue in *Bacillus amyloliquefaciens* subtilisin (i.e., having the same or similar functional capacity to combine, react, or interact chemically).

In order to establish homology to primary structure, the amino acid sequence of a precursor protease is directly compared to the *Bacillus amyloliquefaciens* subtilisin primary sequence and particularly to a set of residues known to be invariant in subtilisins for which sequence is known. For example, Fig. 2 herein shows the conserved residues as between *B. amyloliquefaciens* subtilisin and *B. lenthus* subtilisin. After aligning the conserved residues, allowing for necessary insertions and deletions in order to maintain alignment (i.e., avoiding the elimination of conserved residues through arbitrary deletion and insertion), the residues equivalent to particular amino acids in the primary sequence of *Bacillus amyloliquefaciens* subtilisin are defined. Alignment of conserved residues preferably should conserve 100% of such residues. However, alignment of greater than 75% or as little as 50% of conserved residues is also adequate to define equivalent residues. Conservation of the catalytic triad, Asp32/His64/Ser221 should be maintained.

For example, in Fig. 6 the amino acid sequence of subtilisin from *Bacillus amyloliquefaciens*, *Bacillus subtilis*, *Bacillus licheniformis* (carlsbergensis) and *Bacillus lenthus* are aligned to provide the maximum amount of homology between amino acid sequences. A comparison of these sequences shows that there are a number of conserved residues contained in each sequence. These conserved residues (as between BPN' and *B. lenthus*) are identified in Fig. 2.

These conserved residues, thus, may be used to define the corresponding equivalent amino acid residues of *Bacillus amyloliquefaciens* subtilisin in other subtilisins such as subtilisin from *Bacillus lenthus* (PCT Publication No. W089/06279 published July 25, 1989), the preferred protease precursor enzyme herein, or the subtilisin referred to as PB92 (EP 0 328 299), which is highly homologous to the preferred *Bacillus lenthus* subtilisin. The amino acid sequences of certain of these subtilisins are aligned in Figs. 3A and 3B with the sequence of *Bacillus amyloliquefaciens* subtilisin to produce the maximum homology of conserved residues. As can be seen, there are a number of deletions in the sequence of *Bacillus lenthus* as compared to *Bacillus amyloliquefaciens* subtilisin. Thus, for example, the equivalent amino acid for Val165 in *Bacillus amyloliquefaciens* subtilisin in the other subtilisins is isoleucine for *B. lenthus* and *B. licheniformis*.

Thus, for example, the amino acid at position +170 is lysine (K) in both *B. amyloliquefaciens* and *B. licheniformis* subtilisins and arginine (R) in Savinas. In the protease variants of the invention, however, the amino acid equivalent to +170 in *Bacillus*

amyloliquefaciens subtilisin is substituted with aspartic acid (D). The abbreviations and one letter codes for all amino acids in the present invention conform to the PatentIn User Manual (GenBank, Mountain View, CA) 1990, p.101.

"Equivalent residues" may also be defined by determining homology at the level of 5 tertiary structure for a precursor protease whose tertiary structure has been determined by x-ray crystallography. Equivalent residues are defined as those for which the atomic coordinates of two or more of the main chain atoms of a particular amino acid residue of the precursor protease and *Bacillus amyloliquefaciens* subtilisin (N on N, CA on CA, C on C and O on O) are within 0.13nm and preferably 0.1nm after alignment. Alignment is 10 achieved after the best model has been oriented and positioned to give the maximum overlap of atomic coordinates of non-hydrogen protein atoms of the protease in question to the *Bacillus amyloliquefaciens* subtilisin. The best model is the crystallographic model giving the lowest R factor for experimental diffraction data at the highest resolution available.

15

$$R \text{ factor} = \frac{\sum_h |Fo(h)| - |Fc(h)|}{\sum_h |Fo(h)|}$$

Equivalent residues which are functionally analogous to a specific residue of *Bacillus amyloliquefaciens* subtilisin are defined as those amino acids of the precursor protease which may adopt a conformation such that they either alter, modify or contribute to protein structure, substrate binding or catalysis in a manner defined and attributed to a 20 specific residue of the *Bacillus amyloliquefaciens* subtilisin. Further, they are those residues of the precursor protease (for which a tertiary structure has been obtained by x-ray crystallography) which occupy an analogous position to the extent that, although the main chain atoms of the given residue may not satisfy the criteria of equivalence on the basis of occupying a homologous position, the atomic coordinates of at least two of the 25 side chain atoms of the residue lie with 0.13nm of the corresponding side chain atoms of *Bacillus amyloliquefaciens* subtilisin. The coordinates of the three dimensional structure of *Bacillus amyloliquefaciens* subtilisin are set forth in EPO Publication No. 0 251 446 (equivalent to US Patent 5,182,204, the disclosure of which is incorporated herein by reference) and can be used as outlined above to determine equivalent residues on the 30 level of tertiary structure.

Some of the residues identified for substitution, insertion or deletion are conserved residues whereas others are not. In the case of residues which are not conserved, the replacement of one or more amino acids is limited to substitutions which produce a variant which has an amino acid sequence that does not correspond to one found in nature. In 5 the case of conserved residues, such replacements should not result in a naturally- occurring sequence. The protease variants of the present invention include the mature forms of protease variants, as well as the pro- and prepro-forms of such protease variants. The prepro-forms are the preferred construction since this facilitates the expression, secretion and maturation of the protease variants.

10 "Prosequence" refers to a sequence of amino acids bound to the N-terminal portion of the mature form of a protease which when removed results in the appearance of the "mature" form of the protease. Many proteolytic enzymes are found in nature as translational proenzyme products and, in the absence of post-translational processing, are expressed in this fashion. A preferred prosequence for producing protease variants is the 15 putative prosequence of *Bacillus amyloliquefaciens* subtilisin, although other protease prosequences may be used.

20 A "signal sequence" or "prosequence" refers to any sequence of amino acids bound to the N-terminal portion of a protease or to the N-terminal portion of a proprotease which may participate in the secretion of the mature or pro forms of the protease. This definition of signal sequence is a functional one, meant to include all those amino acid 25 sequences encoded by the N-terminal portion of the protease gene which participate in the effectuation of the secretion of protease under native conditions. The present invention utilizes such sequences to effect the secretion of the protease variants as defined herein. One possible signal sequence comprises the first seven amino acid residues of the signal sequence from *Bacillus subtilis* subtilisin fused to the remainder of the signal sequence of the subtilisin from *Bacillus lentus* (ATCC 21536).

30 A "prepro" form of a protease variant consists of the mature form of the protease having a prosequence operably linked to the amino terminus of the protease and a "pre" or "signal" sequence operably linked to the amino terminus of the prosequence.

35 "Expression vector" refers to a DNA construct containing a DNA sequence which is operably linked to a suitable control sequence capable of effecting the expression of said DNA in a suitable host. Such control sequences include a promoter to effect transcription, an optional operator sequence to control such transcription, a sequence encoding suitable mRNA ribosome binding sites and sequences which control termination of transcription and translation. The vector may be a plasmid, a phage particle, or simply a potential

genomic insert. Once transformed into a suitable host, the vector may replicate and function independently of the host genome, or may, in some instances, integrate into the genome itself. In the present specification, "plasmid" and "vector" are sometimes used interchangeably as the plasmid is the most commonly used form of vector at present.

5 However, the invention is intended to include such other forms of expression vectors which serve equivalent functions and which are, or become, known in the art.

The "host cells" used in the present invention generally are prokaryotic or eukaryotic hosts which preferably have been manipulated by the methods disclosed in US Patent 4,760,025 (RE 34,606) to render them incapable of secreting enzymatically active 10 endoprotease. A preferred host cell for expressing protease is the *Bacillus* strain BG2036 which is deficient in enzymatically active neutral protease and alkaline protease (subtilisin). The construction of strain BG2036 is described in detail in US Patent 5,264,366. Other host cells for expressing protease include *Bacillus subtilis* 1168 (also described in US Patent 4,760,025 (RE 34,606) and US Patent 5,264,366, the disclosure of 15 which are incorporated herein by reference), as well as any suitable *Bacillus* strain such as *B. licheniformis*, *B. lentus*, etc.

Host cells are transformed or transfected with vectors constructed using recombinant DNA techniques. Such transformed host cells are capable of either replicating vectors encoding the protease variants or expressing the desired protease 20 variant. In the case of vectors which encode the pre- or prepro-form of the protease variant, such variants, when expressed, are typically secreted from the host cell into the host cell medium.

"Operably linked," when describing the relationship between two DNA regions, simply means that they are functionally related to each other. For example, a 25 presequence is operably linked to a peptide if it functions as a signal sequence, participating in the secretion of the mature form of the protein most probably involving cleavage of the signal sequence. A promoter is operably linked to a coding sequence if it controls the transcription of the sequence; a ribosome binding site is operably linked to a coding sequence if it is positioned so as to permit translation.

30 The genes encoding the naturally-occurring precursor protease may be obtained in accord with the general methods known to those skilled in the art. The methods generally comprise synthesizing labeled probes having putative sequences encoding regions of the protease of interest, preparing genomic libraries from organisms expressing the protease, and screening the libraries for the gene of interest by hybridization to the probes.

35 Positively hybridizing clones are then mapped and sequenced.

The cloned protease is then used to transform a host cell in order to express the protease. The protease gene is then ligated into a high copy number plasmid. This plasmid replicates in hosts in the sense that it contains the well-known elements necessary for plasmid replication: a promoter operably linked to the gene in question (which may be supplied as the gene's own homologous promoter if it is recognized, i.e., transcribed, by the host), a transcription termination and polyadenylation region (necessary for stability of the mRNA transcribed by the host from the protease gene in certain eucaryotic host cells) which is exogenous or is supplied by the endogenous terminator region of the protease gene and, desirably, a selection gene such as an antibiotic resistance gene that enables continuous cultural maintenance of plasmid-infected host cells by growth in antibiotic-containing media. High copy number plasmids also contain an origin of replication for the host, thereby enabling large numbers of plasmids to be generated in the cytoplasm without chromosomal limitations. However, it is within the scope herein to integrate multiple copies of the protease gene into host genome. This is facilitated by prokaryotic and eucaryotic organisms which are particularly susceptible to homologous recombination.

In one embodiment, the gene can be a natural gene such as that from *B. lentus* or *B. amyloliquefaciens*. Alternatively, a synthetic gene encoding a naturally-occurring or mutant precursor protease may be produced. In such an approach, the DNA and/or amino acid sequence of the precursor protease is determined. Multiple, overlapping synthetic single-stranded DNA fragments are thereafter synthesized, which upon hybridization and ligation produce a synthetic DNA encoding the precursor protease. An example of synthetic gene construction is set forth in Example 3 of US Patent 5,204,015, the disclosure of which is incorporated herein by reference.

Once the naturally-occurring or synthetic precursor protease gene has been cloned, a number of modifications are undertaken to enhance the use of the gene beyond synthesis of the naturally-occurring precursor protease. Such modifications include the production of recombinant proteases as disclosed in US Patent 4,760,025 (RE 34,606) and EPO Publication No. 0 251 446 and the production of protease variants described herein.

The following cassette mutagenesis method may be used to facilitate the construction of the protease variants of the present invention, although other methods may be used. First, the naturally-occurring gene encoding the protease is obtained and sequenced in whole or in part. Then the sequence is scanned for a point at which it is desired to make a mutation (deletion, insertion or substitution) of one or more amino acids

in the encoded enzyme. The sequences flanking this point are evaluated for the presence of restriction sites for replacing a short segment of the gene with an oligonucleotide pool which when expressed will encode various mutants. Such restriction sites are preferably unique sites within the protease gene so as to facilitate the replacement of the gene segment. However, any convenient restriction site which is not overly redundant in the protease gene may be used, provided the gene fragments generated by restriction digestion can be reassembled in proper sequence. If restriction sites are not present at locations within a convenient distance from the selected point (from 10 to 15 nucleotides), such sites are generated by substituting nucleotides in the gene in such a fashion that neither the reading frame nor the amino acids encoded are changed in the final construction. Mutation of the gene in order to change its sequence to conform to the desired sequence is accomplished by M13 primer extension in accord with generally known methods. The task of locating suitable flanking regions and evaluating the needed changes to arrive at two convenient restriction site sequences is made routine by the redundancy of the genetic code, a restriction enzyme map of the gene and the large number of different restriction enzymes. Note that if a convenient flanking restriction site is available, the above method need be used only in connection with the flanking region which does not contain a site.

Once the naturally-occurring DNA or synthetic DNA is cloned, the restriction sites flanking the positions to be mutated are digested with the cognate restriction enzymes and a plurality of end termini-complementary oligonucleotide cassettes are ligated into the gene. The mutagenesis is simplified by this method because all of the oligonucleotides can be synthesized so as to have the same restriction sites, and no synthetic linkers are necessary to create the restriction sites.

In one aspect of the invention, the objective is to secure a variant protease having altered allergenic potential as compared to the precursor protease, since decreasing such potential enables safer use of the enzyme. While the instant invention is useful to lower allergenic potential, the mutations specified herein may be utilized in combination with mutations known in the art to result altered thermal stability and/or altered substrate specificity, modified activity or altered alkaline stability as compared to the precursor.

Thus, in combination with the mutations of the present invention, substitutions at positions corresponding to N76D/S103A/V104I/G159D optionally in combination with one or more substitutions selected from the group consisting of positions corresponding to V68A, T213R, A232V, Q236H, Q245R, and T260A of *Bacillus amyloliquefaciens* subtilisin may be used, in addition to decreasing the allergenic potential of the variant protease of

the invention, to modulate overall stability and/or proteolytic activity of the nzym . Similarly, the substitutions provided herein may be combined with mutation at the Asparagine (N) in *Bacillus lenthus* subtilisin at equivalent position +76 to Aspartate (D) in combination with the mutations S103A/V104I/G159D and optionally in combination with 5 one or more substitutions selected from the group consisting of positions corresponding to V68A, T213R, A232V, Q236H, Q245R, and T260A of *Bacillus amyloliquefaciens* subtilisin, to produce enhanced stability and/or enhanced activity of the resulting mutant enzyme.

Based on the screening results obtained with the variant proteases, the noted 10 mutations in *Bacillus amyloliquefaciens* subtilisin are important to the proteolytic activity, performance and/or stability of these enzymes and the cleaning or wash performance of such variant enzymes.

Many of the protease variants of the invention are useful in formulating various 15 detergent compositions. A number of known compounds are suitable surfactants useful in compositions comprising the protease mutants of the invention. These include nonionic, anionic, cationic, anionic or zwitterionic detergents, as disclosed in US 4,404,128 to Barry J. Anderson and US 4,261,868 to Jiri Flora, et al. A suitable detergent formulation is that described in Example 7 of US Patent 5,204,015 (previously incorporated by reference). The art is familiar with the different formulations which can be used as cleaning 20 compositions. In addition to typical cleaning compositions, it is readily understood that the protease variants of the present invention may be used for any purpose that native or wild-type proteases are used. Thus, these variants can be used, for example, in personal care items such as face lotions and cosmetics, in bar or liquid soap applications, dishcare 25 formulations, contact lens cleaning solutions or products, peptide hydrolysis, waste treatment, textile applications, as fusion-cleavage enzymes in protein production, etc. The variants of the present invention may comprise enhanced performance in a detergent composition (as compared to the precursor). As used herein, enhanced performance in a detergent is defined as increasing cleaning of certain enzyme sensitive stains such as grass or blood, as determined by usual evaluation after a standard wash cycle.

Proteases of the invention can be formulated into known powdered and liquid 30 detergents having pH between 6.5 and 12.0 at levels of about .01 to about 5% (preferably .1% to .5%) by weight. These detergent cleaning compositions can also include other enzymes such as known proteases, amylases, cellulases, lipases or endoglycosidases, as well as builders and stabilizers.

The addition of proteases of the invention to conventional cleaning compositions 35 does not create any special use limitation. In other words, any temperature and pH

suitable for the detergent is also suitable for the present compositions as long as the pH is within the above range, and the temperature is below the described protease's denaturing temperature. In addition, proteases of the invention can be used in a cleaning composition without detergents, again either alone or in combination with builders and 5 stabilizers.

The variant proteases of the present invention can be included in animal feed such as part of animal feed additives as described in, for example, US 5,612,055; US 5,314,692; and US 5,147,642.

One aspect of the invention is a composition for the treatment of a textile that 10 includes variant proteases of the present invention. The composition can be used to treat for example silk or wool as described in publications such as RD 216,034; EP 134,267; US 4,533,359; and EP 344,259.

The following is presented by way of example and is not to be construed as a limitation to the scope of the claims.

15 All publications and patents referenced herein are hereby incorporated by reference in their entirety.

EXAMPLES

Example 1

20 Assay for the Identification of Peptide T-Cell Epitopes
Using Naïve Human T-Cells

Fresh human peripheral blood cells were collected from "naïve" humans, i.e., persons not known to be exposed to or sensitized to *Bacillus licheniformis* protease, for determination of antigenic epitopes in protease from *Bacillus licheniformis* and human subtilisin. 25 Naïve humans is intended to mean that the individual is not known to have been exposed to or developed a reaction to protease in the past. Peripheral mononuclear blood cells (stored at room temperature, no older than 24 hours) were prepared for use as follows: Approximately 30 mls of a solution of buffy coat preparation from one unit of whole blood was brought to 50 ml with Dulbecco's phosphate buffered solution (DPBS) and split into 30 two tubes. The samples were underlaid with 12.5 ml of room temperature lymphoprep density separation media (Nycomed density 1.077 g/ml). The tubes were centrifuged for thirty minutes at 600G. The interface of the two phases was collected, pooled and washed in DPBS. The cell density of the resultant solution was measured by hemocytometer. Viability was measured by trypan blue exclusion.

From the resulting solution, a differentiated dendritic cell culture was prepared from the peripheral blood mononuclear cell sample having a density of 10^8 cells per 75 ml culture flask in a solution as follows:

(1) 50 ml of serum free AIM V media (Gibco) was supplemented with a

5 1:100 dilution beta-mercaptoethanol (Gibco). The flasks were laid flat for two hours at 37°C in 5% CO₂ to allow adherence of monocytes to the flask wall.

(2) Differentiation of the monocyte cells to dendritic cells was as follows: nonadherent cells were removed and the resultant adherent cells (monocytes) combined with 30 ml of AIM V, 800 units/ml of GM-CSF (Endogen) 10 and 500 units/ml of IL-4 (Endogen); the resulting mixture was cultured for 5 days under conditions at 37°C in 5% CO₂. After five days, the cytokine TNF(α) (Endogen) was added to 0.2 units/ml, and the cytokine IL-1α (Endogen) was added to a final concentration of 50 units/ml and the mixture incubated at 37°C in 5% CO₂ for two more days.

15 (3) On the seventh day, Mitomycin C was added to a concentration of 50 microgram/ml was added to stop growth of the now differentiated dendritic cell culture. The solution was incubated for 60 minutes at 37°C in 5% CO₂. Dendritic cells were collected by gently scraping the adherent cells off the bottom of the flask with a cell scraper. Adherent and non-adherent cells were then centrifuged at 20 600G for 5 minutes, washed in DPBS and counted.

(4) The prepared dendritic cells were placed into a 96 well round bottom array at 2×10^4 /well in 100 microliter total volume.

CD4+ T cells were prepared from frozen aliquots of the peripheral blood cell samples used to prepare the dendritic cells using the human CD4+ Cellect Kit (Biotex) as 25 per the manufacturers instructions with the following modifications: the aliquots were thawed and washed such that approximately 10^8 cells will be applied per Cellect column; the cells were resuspended in 4 ml DPBS and 1 ml of the Cell reagent from the Cellect Kit, the solution maintained at room temperature for 20 minutes. The resultant solution was centrifuged for five minutes at 600G at room temperature and the pellet resuspended in 30 2 ml of DPBS and applied to the Cellect columns. The effluent from the columns was collected in 2% human serum in DPBS. The resultant CD4+ cell solution was centrifuged, resuspended in AIMV media and the density counted.

The CD4+ T-cell suspension was resuspended to a count of 2×10^6 /ml in AIM V media to facilitate efficient manipulation of the 96 well plate.

P peptide antigen is prepared from a 1M stock solution in DMSO by dilution in AIM V media at a 1:10 ratio. 10 microliters of the stock solution is placed in each well of the 96 well plate containing the differentiated dendritic cells. 100 microliter of the diluted CD4+ T-cell solution as prepared above is further added to each well. Useful controls include 5 diluted DMSO blanks, and tetanus toxoid positive controls.

The final concentrations in each well, at 210 microliter total volume are as follows:

2x10⁵ CD4+

2x10⁴ dendritic cells (R:S of 10:1)

5 mM/10⁴ peptide

10

Example 2

Identification of T-Cell Epitopes in Protease from *Bacillus lenthus* and Human subtilisin

Peptides for use in the assay described in Example 1 were prepared based on the 15 *Bacillus lenthus* and human subtilisin amino acid sequence. Peptide antigens were designed as follows. From the full length amino acid sequence of either human subtilisin or *Bacillus lenthus* protease provided in Figure 1, 15mers were synthetically prepared, each 15mer overlapping with the previous and the subsequent 15mer except for three residues.

Peptides used correspond to amino acid residue strings in *Bacillus lenthus* as 20 provided in Figure 7, and peptides correspond to amino acid residues in human subtilisin as provided in Figure 8. The key for the coded results is provided in Figure 10. All tests were performed at least in duplicate. All tests reported displayed robust positive control responses to the antigen tetanus toxoid. Responses were averaged within each experiment, then normalized to the baseline response. A positive event was recorded if 25 the response was at least 3 times the baseline response.

The immunogenic response (i.e., T-cell proliferation) to the prepared peptides from 30 human subtilisin and *Bacillus lenthus* was tallied and is provided in Figures 4 and 5, respectively. T-cell proliferation was measured by the incorporated tritium method. The results shown in Figures 4 and 5 as a comparison of the immunogenic additive response in 10 individuals (figure 4) and 16 individuals (figure 5) to the various peptides. Response is indicated as the added response wherein 1.0 equals a baseline response for each sample. Thus, in Figure 4, a reading of 10.0 or less is the baseline response and in Figure 5 a reading of 16.0 or less the baseline response.

As indicated in Figures 4 and 5, the immunogenic response of the naïve blood samples from unsensitized individuals showed a marked allergenic response at the peptide fragment from *Bacillus lenthus* corresponding to residues 170-173 of *Bacillus amyloliquefaciens* protease. As expected, the corresponding fragment in human subtilisin 5 evokes merely baseline response.

WE CLAIM:

1. A method for reducing the allergenicity of a non-human protein is provided wherein an epitope is identified and replaced with an analogous region within a human subtilisin.

5 2. The method according to claim 1, wherein said non-human protein comprises a protease.

3. The method according to claim 2, wherein said epitope replaced is a T-cell epitope.

10 4. A method for producing the protein of the invention having reduced allergenicity comprising, preparing a mutant protein by modifying a DNA encoding a precursor protein so that the modified DNA encodes the mutant protein of the invention, wherein an epitope is replaced with an analogous region from human subtilisin.

5. A mutant protein having reduced allergenicity produced according to the method of claim 4.

15 6. DNA encoding the mutant protein of claim 5.

7. An expression vector containing a DNA sequence according to claim 6.

8. Host cells transformed with the vectors of claim 7.

9. A method of producing a protein having reduced allergenicity wherein the host cells of claim 8 are cultivated under conditions which result in expression of the mutant protease.

20 10. A pharmaceutical composition comprising a human subtilisin.

11. A DNA encoding a human subtilisin.

12. A vector comprising the DNA of claim 11.

13. A host cell comprising the vector of claim 12.

25 14. A human subtilisin produced by the host cell of claim 12.

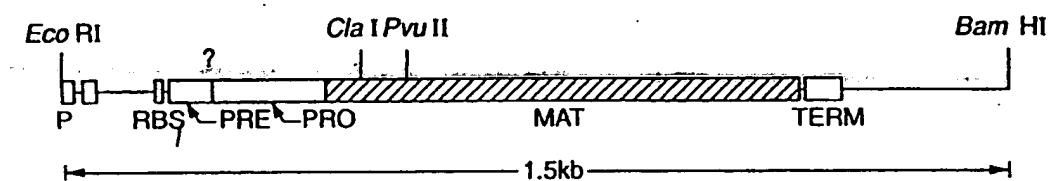


FIG. 1A

1	P	GGTCTACTAAATTATTCATACTATACTTAAACAGAATAATCTGCTATGGTTTCTGAAATGAAAAGGAGGATAAAGA	GTG	RBS	-107	
99	Arg	Gly Lys Lys Val Thr Ile Ser Leu Phe Ala Leu Ala Phe Thr Met Ala Phe Gly Ser Thr Ser			Met	
99	AGA	GGC AAA GTC TGG ATC AGT TCG	GGC AGC ACA TCG TTT GCT TTA ATC TTT ACG ATG GCG TTC GGC AGC ACA TCC			
174	Ser	Ala Glu Ala Ala Glu Lys Ser Asn Glu Glu Lys Tyr Ile Val Gly Phe Lys Glu Thr Met Ser Thr Met				
174	TCT	GCC CAG GCG GCA GGG AAA TCA AAC GGG GAA AAG AAA TCA AAC GGG AAC AAG AAA TAT ATT GTC GAA TTC AAA TAT GCA ATG AGC ACG ATG ATG				
249	Ser	Ala Ala Lys Lys Lys Asp Val Ile Ser Glu Glu Lys Gly Lys Val Lys Glu Pro Ser Val Ala Tyr Val Glu Asp				
249	AGC GCG GCT AAG AAG AAA GAT GTC ATT TCT GAA AAA GGC GGG AAA GTG CAA TTC AAA GAC CCG AGC GTC GCT TAC GTT GAA GAT					
324	Ala	Ser Ala Thr Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Asp Pro Ser Val Ala Tyr Val Glu Asp				
324	GCT TCA GCT ACA AAC GAA AAA GCT GTC AAA GAA TTG AAA GAC GTC GCT TAC GGC CCT GCT TAC GTC CAC TCT CAA					
399	His	Val Ala His Ala Tyr Ala Glu Ser Val Pro Tyr Gly Val Ser Glu Ile Lys Ala Pro Ala Leu His Ser Glu				
399	CAC GTA GCA CAT GCG TAC GCG CAG TCC GTG CCT TAC GGC GTA TCA CAA ATT AAA GCC CCT GCT CTG CAC TCT CAA					
474	Gly	Ty Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp Ser Gly Ile Asp Ser His Ser His Pro Asp Leu Lys Val				
474	GGC TAC ACT GGA TCA ATT GTT AAA GTC GCT ATC GAC AGC GGT ATC GAT TCT CAT CCT GAT TTA AAG GTC					

FIG. 1B - 1

549	Ala	Gly	Gly	Ala	Ser	Met	Val	Pro	Ser	Glu	Thr	Asn	Pro	Asn	Asp	Asn	Ser	Gly	Thr	His	Val	Ala		
	GCA	GGC	GGG	GCA	GCC	AGC	ATG	GTT	CCT	TCT	GAA	ACA	AAT	CCT	TTC	CAA	GAC	AAC	TCT	CAC	GGA	ACT	CAC	
560	Gly	Thr	Val	Ala	Ala	Leu	Asn	Asn	Val	Gly	Val	Leu	Gly	Val	Ala	Pro	Ser	Ala	Ser	Leu	Trp	Ala	Val	
	GGC	ACA	GTT	GCG	GCT	CCT	AAT	AAC	TCA	ATC	GGT	GTA	TTA	GCC	GTT	GCG	CCA	AGC	GCA	GCA	TCA	CTT	TAC	
570	Asp	Ala	Asp	Ala	Asp	Gly	Ser	Gly	Ile	Gly	Val	Leu	Gly	Val	Ala	Pro	Ser	Ala	Ser	Ala	90			
	GGT	CCT	GGT	GCT	GAC	GGT	TCC	GGC	CAA	TAC	ATC	GGC	ATC	ATC	GGT	ATC	GAG	TGG	GCG	ATC	GCA	AAC	AAT	
580	Val	Leu	Gly	Ala	Asp	Gly	Ser	Gly	Gly	Asn	Val	Ile	Asn	Gly	Ile	Glu	Trp	Ala	Ile	Ala	Asn	Asn	Lys	
	624																							
590	Asp	Val	Ile	Asn	Met	Ser	Leu	Gly	Gly	Pro	Ser	Ala	Ala	Leu	Lys	Ala	Ala	Val	Asp	Lys	Ala	Val	Ala	
	669																							
600	Asp	Val	Ile	Asn	Met	Ser	Leu	Gly	Gly	Pro	Ser	Gly	Ser	Ala	Leu	Lys	Ala	Ala	Val	Ile	Ala	Asn	Met	
	774																							
610	Asp	Val	Ile	Asn	Met	Ser	Leu	Gly	Gly	Pro	Ser	Gly	Ser	Ala	Leu	Lys	Ala	Ala	Val	Ile	Ala	Asn	Met	
	774																							
620	GAC	GTT	ATT	AAC	ATG	AGC	CTC	GGC	GGG	CCT	TCT	GGT	TCT	GCT	GCT	GCT	GCA	GCG	GAT	AAA	GCC	GCC	GTT	
630	Ser	Gly	Val	Val	Val	Ala	Ala	Ala	Gly	Asn	Glu	Gly	Ser											
	849																							
640	Ser	Gly	Val	Val	Val	Ala	Ala	Ala	Gly	Asn	Glu	Gly	Val	Thr	Ser									
	849																							
650	Ser	Gly	Val	Val	Val	Ala	Ala	Ala	Gly	Asn	Glu	Gly	Val	Thr	Ser									
	849																							
660	Ser	Gly	Val	Val	Val	Ala	Ala	Ala	Gly	Asn	Glu	Gly	Val	Thr	Ser									
	849																							
670	Lys	Tyr	Pro	Ser	Val	Ile	Ala	Val	Gly	Ala	Val	Asp	Ser	Ser	Asn	Gln	Ala	Ser	Phe	Ser	Ser	Val	Gly	
	924																							
680	AAA	TAC	CCT	TCT	GTC	ATT	GCA	GTA	GGC	GCT	GTT	GAC	AGC	AAC	AGC	CAA	AGA	CAA	TCT	TTC	TCA	AGC	GTA	GGA
690	Glu	Leu	Asp	Val	Met	Ala	Pro	Gly	Val	Ser	Ile	Gln	Ser	Thr	Leu	Phe	Gly	Asn	Lys	Tyr	Ala	Tyr	Asn	Gly
	999																							
700	GAG	CTT	GAT	GTC	ATG	GCA	CCT	GGC	GTA	TCT	ATC	CAA	AGC	AGC	CTT	CCT	GGG	AAC	AAA	TAC	GGG	GGG	TAC	AAC
710	Asn	Thr	Ser	Met	Ala	Ser	Pro	Gly	Val	Ala	Gly	Asn	Val	Leu	Ile	Leu	Ser	Lys	His	Phe	Ser	Val	Asn	Thr
	1074																							
720	1074	ACG	TCA	ATG	GCA	TCR	CCG	CAC	GTT	GCC	GGA	GCT	GCT	TTC	TCT	AGG	CAC	CCG	AAC	TGG	ACA	AAC	ACT	

FIG.-1B - 2

250 Gln Val Arg Ser Ser 250 Gln
Gln Val GTC CGC AGC AGT TTA GAA AAC ACC ACT ACA AAA CTT GAT GGT TCT TAC TAC TAC TAC TAC AAC
1149 CAA GTC CGC AGC AGT TTA GAA AAC ACC ACT ACA AAA CTT GAT GGT TCT TAC TAC TAC TAC TAC AAC

270 Val Gln Ala Ala 275 Gln OC TERM
1224 GTA CAG GCG GCA GCT CAG TAA MACATAAAAACCGCCGTTT GCTCCCGCCGGGGTTTATTTCTCCCGCATGTTCAAATCCGGTCC

1316 ATATCGACGGATGGCTCCCTCTGAAAAATTAAACGAGAACGGGAAACGGGAAACGGGCTCAGTCCGTAACGGCCAGTCCCTGAAACGTCATACTGGCG

1416 CTTCGGGTTCCGGTCAAGCTCAATGCCGTAACGGTCCGGCTTCCGTAAACGGGAGACGGGATTCTGTAATCGGATC

FIG._ 1B - 3

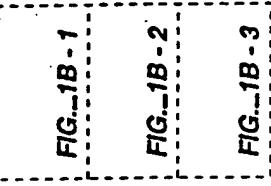


FIG._ 1B

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CONSERVED RESIDUES IN SUBTILISINS FROM
BACILLUS AMYLOLIQUEFACIENS

1 10 20
A Q S V P . G A P A . H . . G

21 30 40
. T G S . V K V A V . D . G H P

41 50 60
D L . . . G G A S . V P Q D

61 70 80
. N . H G T H V A G T . A A L N N S I G

81 90 100
V L G V A P S A . L Y A V K V L G A . G

101 110 120
S G . . S . L . . G . E W A . N . . .

121 130 140
V . N . S L G . P S . S A . .

141 150 160
. G V . V V A A . G N . G . . .

161 170 180
. Y P . . Y A V G A .

181 190 200
D . . N . . A S P S . . G . . L D . . A

201 210 220
P G V . . Q S T . P G . . Y . . . N G T

221 230 240
S M A . P H V A G A A A L . . . K . . .

241 250 260
W . . . Q . R . . L . N T . . . L G . . .

261 270
. . Y G . G L . N . . A A . .

FIG. 2

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COMPARISON OF SUBTILISIN SEQUENCES FROM:
B.amyloliquefaciens
B.subtilis
B.licheniformis
B.lentus

01	A Q S V P Y G V S Q I K A P A L H S Q G Y T G S N V K V A V I D S G I D S S H P	20	A Q S V P Y G I S Q I K A P A L H S Q G Y T G S N V K V A V I D S G I D S S H P	30	A Q T V P Y G I P L I K A D K V Q A Q G F K G A N V K V A V L D T G I Q A S H P		
	A Q S V P Y G I P L I K A D K V Q A Q G F K G A N V K V A V L D T G I Q A S H P		A Q S V P Y G I S R V Q A P A A H N R G L T G S G V K V A V L D T G I S T * H P				
41	D L K V A G G A S M V P S E T N P P Q D N N S H G T H V A G T V A A L N N S I G	50	D L N V R G G A S P V P S E T N P Y Q D G S S H G T H V A G T I A A L N N S I G	60	D L N V V G G A S P V V A G E A Y N * T D G N G H G T H V A G T V A A L D N T T G		
	D L N T R G G A S P V P G E * P S T Q D G N G H G T H V A G T I A A L N N S I G		D L N T R G G A S P V P G E * P S T Q D G N G H G T H V A G T I A A L N N S I G				
81	V L G V A P S A S L Y A V K V L G A D G Q Y S W I I N G I E W A I A N N M D	90	V L G V S P S A S L Y A V K V L D S T G S G Q Y S W I I N G I E W A I S N N M D	100	V L G V A P S V S L Y A V K V L N S S G S G S Y S G I V S G I V S G S V S S I A Q G L E W A G N N G M D	110	V L G V A P S A E L Y A V K V L G A S G S G S V S S I A Q G L E W A G N N G M D
121	V I N M S L G G G P S G S A A L K A A V D K A V A S G V V V V A A G N E G T S G	130	V I N M S L G G P T G S T A L K T V V D K A V S S G I V V A A A G N E G S S G	140	V I N M S L G G C A S G S T A M K Q A V D N A Y A R G V V V V A A A G N S G N S C	150	V A N L S L G S P S P S A T L E Q A V N S A T S R G V L V V A A S G N S G A G S

FIG.-3A

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FIG. - 3B

FIG. 3

FIG.-3B

5G 34

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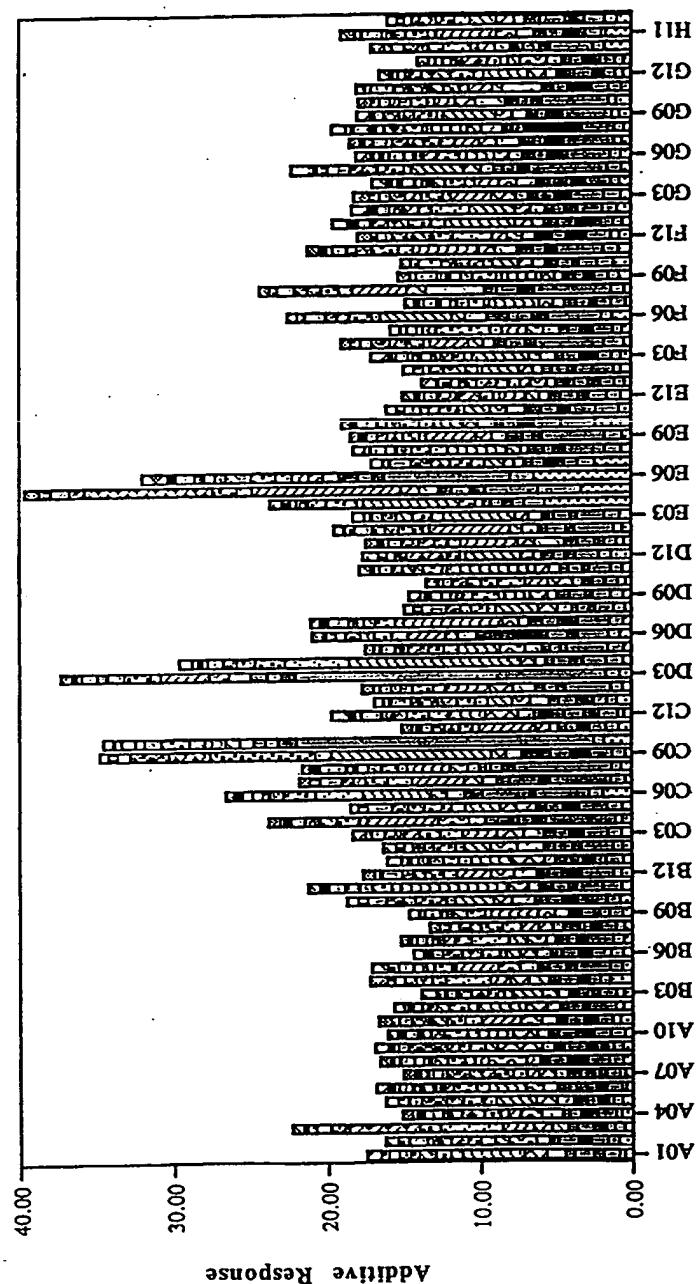


FIG. 4

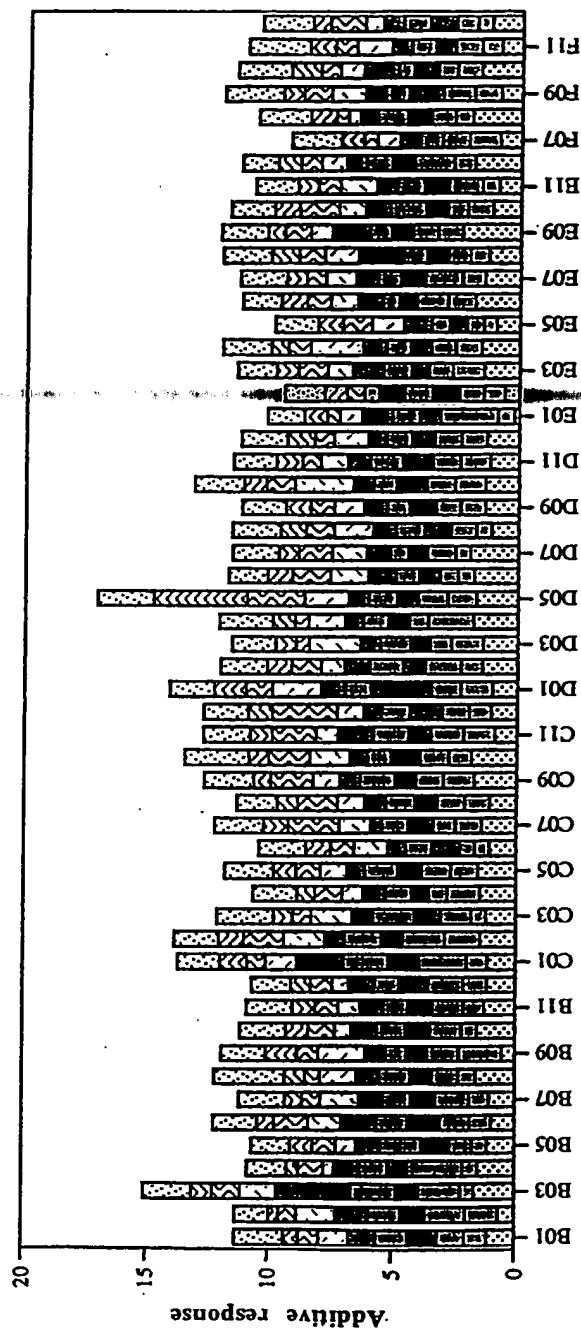


FIG. 5

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MKLVNIWLLLvvLLCGKHLGDRLEKKSFEKAPCPGCSHLTLKVEFSSTVVEYEYIVAFNGYFT
AKARNSFISSALKSSEVDNWRRIIPRNNPSSDYPDSDFEVIQIKEKQKAGLLTLEDHPNIKRVTQQR
KVFRSLKYAEDPTVPCNETRWSQWQSSRPLRRASLSCSGFWHATGRHSSRLLRAIPRQVAQ
TLQADVLWQMGTGANVRVAVFDTGLSEKHPHFKNVKERTNWTNERTLDDGLGHGTFVAGVIASM
RECQGFAPDAELHIFRVFTNNQVSYTWSFLDAFNAYAILKKIDVLNLSIGGPDFMDHPFVDKVWEL
TANNVIMVSAIGNDGPLYGTLNNPADQMDVIGVGGIDFEDNIARFSSRGMTTWELPGGYGRMKPD
IVTYGAGVRGSGVKGGCRALSGTSVAPVAVGATLLVSTVQKRELVNPASMKQALIASARRLPG
VNMFEQGHGKLDLLRAYQILNSYKPQASLSPSYIDLTECPYMWPYCSQPIYYGGMPTVNVNTILN
GMGVTGRIVDKPDWQPYLPQNGDNIEVAFSYSSVLWPWSGYLAISISVTKKAASWEGIAQGHVMI
TVASPAETESKNGAEQTSTVKLPIKVIIPTPPRSKRLWDQYHNLRYPPGYFPRDNLRMKNDPL
DWNGDHIHTNFRDMYQHLRSMGYFVEVLGAPFTCFDASQYGTLLMVDSEEEYFPEEIAKLRDV
NGLSLVIFSDWYNTSVMRKVKFYDENTRQWWMPDTGGGANIPALNELLSVWNMGFSDGLEYGEFTL
ANHDMDYYASGCSIAKFPEDGVVITQTFKDQGLEVLKQETAVVENVPILGLYQIPAEGGGRIVLYG
DSNCLDDSHRQKDCFWLLDALLQYTSYGVTPPSLHSGNRQRPPSGAGSVTPERMEGNHLHRYSK
VLEAHLGDPKPRPLPACPRLSWAKPQPLNETAPSNLWKHQKLLSIDLDKVVLPNFRSNRPQVRPL
SPGESGAWDIPGGIMPGRYNQEVGQTIPVFAFLGAMVVLAFFVVQINKAKSRPKRRKPRVKRQPL
MQQVHPPKTPSV

FIG. 6

1	A12	IKDFHVYFRESRDA	49	E12	SATSRGVLVVAASGN
2	A11	LEQAVNSATSRGVLV	50	E11	SRGVLVVAASGNSGA
3	A10	AQSVPWGISRQAPA	51	E10	VLVVAASGNSGAGSI
4	A9	VPWGISRQAPAHHN	52	E9	VAASGNSGAGSISYP
5	A8	GISRVQAPAHHNRGL	53	E8	SGNSGAGSISYPARY
6	A7	RVQAPAHHNRGLTGS	54	E7	SGAGSISYPARYANA
7	A6	APAAHNRLTGSGVK	55	E6	GSISYPARYANAMAV
8	A5	AHNRLTGSGVKAVAV	56	E5	SYPARYANAMAVGAT
9	A4	RGLTGSGVKAVLDT	57	E4	ARYANAMAVGATDQN
10	A3	TGSGVKAVLDTGIS	58	E3	ANAMAVGATDQNNR
11	A2	GVKAVLDTGISTHP	59	E2	MAVGATDQNNNRASF
12	A1	VAVLDTGISTHPDLN	60	E1	GATDQNNNRASFQY
13	B12	LDTGISTHPDLNIRG	61	F12	DQNNNRASFQYGAG
14	B11	GISTHPDLNIRGGAS	62	F11	NNRASFQYGAGLDI
15	B10	THPDLNIRGGASFVP	63	F10	ASFSQYGAGLDIVAP
16	B9	DLMIRGGASFVPGEP	64	F9	SQYGAGLDIVAPGVN
17	B8	IRGGASFVPGEPSTQ	65	F8	GAGLDIVAPGVNVQS
18	B7	GASFVPGEPSTQDGN	66	F7	LDIVAPGVNVQSTYP
19	B6	FVPGEPESTQDGNGHG	67	F6	VAPGVNVQSTYPGST
20	B5	GEPESTQDGNGHGTHV	68	F5	GVNVQSTYPGSTYAS
21	B4	STQDGNGHGTHVAGT	69	F4	VQSTYPGSTYASLNG
22	B3	DGNHGHTHVAGTIAA	70	F3	TPGSTYASLNGTSM
23	B2	GHGHTHVAGTIAALNN	71	F2	GSTYASLNGTSMATP
24	B1	THVAGTIAALNNSIG	72	F1	YASLNGTSMATPHVA
25	C12	AGTIAALNNSIGVLG	73	G12	LNGTSMATPHVAGAA
26	C11	IAALNNSIGVLGVAP	74	G11	TSMATPHVAGAAALV
27	C10	LNNNSIGVLGVAPSAE	75	G10	ATPHVAGAAALVKQK
28	C9	SIGVLGVAPSAELYA	76	G9	HVAGAAALVKQKNPS
29	C8	VLGVAPSAELYAVKV	77	G8	GAAALVKQKNPSWSN
30	C7	VAPSAELYAVKVLGA	78	G7	ALVKQKNPSWSNVQI
31	C6	SAELYAVKVLGASGS	79	G6	KQKNPSWSNVQIRNH
32	C5	LYAVKVLGASGSGSV	80	G5	NPSWSNVQIRNLKN
33	C4	VKVLGASGSGSVSSI	81	G4	WSNVQIRNLKNTAT
34	C3	LGASGSGSVSSIAQG	82	G3	VQIRNLKNTATSLG
35	C2	SGSGSVSSIAQGLEW	83	G2	RNHLKNTATSLGSTN
36	C1	GSVSSIAQGLEWAGN	84	G1	LKNTATSLGSTNLYG
37	D12	SSIAQGLEWAGNNGM	85	H12	TATSLGSTNLYGSGL
38	D11	AQGLEWAGNNGMHVA	86	H11	SLGSTNLYGSGLVNA
39	D10	LEWAGNNGMHVA	87	H10	STNLYGSGLVNAEAA
40	D9	AGNNGMHVANLSLGS	88	H9	NLYGSGLVNAEATR
41	D8	NGMHVANLSLGS			
42	D7	HVANLSLGS			
43	D6	NLSLGS			
44	D5	LGSPSPSAT			
45	D4	PSPSAT			
46	D3	SAT			
47	D2	LEQAVNSATS			
48	D1	AVNSATS			

FIG. 7

1	A12	IKDFHVYFRESRDA	49	E12	KKIDVLNLSIGGPDF
2	A11	DAELHIFRVFTNNQV	50	E11	DVLNLSIGGPDFMDH
3	A10	PLRRASLSLGSGFWH	51	E10	NLSIGGPDFMDHPFV
4	A9	RASLSLGSGFWHATG	52	E9	IGGPDFMDHPFVDKV
5	A8	LSLGSGFWHATGRHS	53	E8	PDFMDHPFVDKVWEL
6	A7	GSGFWHATGRHSSRR	54	E7	MDHPFVDKVWELTAN
7	A6	FWHATGRHSSRRLLR	55	E6	PFVDKVWELTANNVI
8	A5	ATGRHSRRLLRAIP	56	E5	DKWELTANNVIMVS
9	A4	RHSSRRLLRAIPRQV	57	E4	WELTANNVIMVSAIG
10	A3	SRRLLRAIPRQVAQT	58	E3	TANNVIMVSAIGNDG
11	A2	LLRAIPRQVAQTLQA	59	E2	NVIMVSAIGNDGPLY
12	A1	AIPRQVAQTLQADVL	60	E1	MVSAIGNDGPLYGTJ
13	B12	RQVAQTLQADVLWQM	61	F12	AIGNDGPLYGTLNNP
14	B11	AQTLQADVLWQMGT	62	F11	NDGPLYGTLNNPADQ
15	B10	LQADVLWQMGTGAN	63	F10	PLYGTLNNPADQMDV
16	B9	DVLWQMGTGANVRV	64	F9	GTLNTPADQMDVIGV
17	B8	WQMGTGANVRVAVF	65	F8	NNPADQMDVIGVGGI
18	B7	GYTGANVRVAVFDTG	66	F7	ADQMDVIGVGGIDFE
19	B6	GANVRVAVFDTGLSE	67	F6	MDVIGVGGIDFEDNI
20	B5	VRVAVFDTGLSEKHP	68	F5	IGVGGIDFEDNIARF
21	B4	AVFDTGLSEKHPFK	69	F4	GGIDFEDNIARFSSR
22	B3	DTGLSEKHPFKNVK	70	F3	DFEDNIARFSSRGMT
23	B2	LSEKHPFKNVKERT	71	F2	DNIARFSSRGMTTWE
24	B1	KHHPFKNVKERTNWT	72	F1	ARFSSRGMTTWEPLG
25	C12	HFKNVKERTNWTNER	73	G12	SSRGMTTWEPLGGY
26	C11	NVKERTNWTNERLTD	74	G11	GMTTWEPLGGYGRMK
27	C10	ERTNWTNERLDDGL	75	G10	TWELPGGYGRMKPDI
28	C9	NWTNERTLDDGLGHG	76	G9	LPGGYGRMKPDIVTY
29	C8	NERTLDDGLGHGTFV	77	G8	GYGRMKPDIVTYGAG
30	C7	TLDDGLGHGTFVAGV	78	G7	RMKPDIVTYGAGVRG
31	C6	DGLGHGTFVAGVIAS	79	G6	PDIVTYGAGVRGSGV
32	C5	GHGTTFVAGVIASMRE	80	G5	VTYGAGVRGSGVKGG
33	C4	TFVAGVIASMRECOQ	81	G4	GAGVRGSGVKGGCRA
34	C3	AGVIASMRECOQFAP	82	G3	VRGSGVKGGCRALSG
35	C2	IASMRECQGFAPDAE	83	G2	SGVKGGCRALSGTSV
36	C1	MRECQGFAPDAELHI	84	G1	KGGCRALSGTSVASP
37	D12	CQGFAPDAELHIFRV	85	H12	CRALSGTSVASPVVA
38	D11	FAPDAELHIFRVFTN	86	H11	LSGTSVASPVAGAV
39	D10	DAELHIFRVFTNNQV	87	H10	TSVASPVAGAVTLL
40	D9	LHIFRVFTNNQVSYT	88	H9	ASPVVAGAVTLLVST
41	D8	FRVFTNNQVSYTWSF	89	H8	VVAGAVTLLVSTVQK
42	D7	FTNNQVSYTWSFLDA	90	H7	GAVTLLVSTVQKREL
43	D6	NQVSYTWSFLDAFNY	91	H6	TLLVSTVQKRELVNP
44	D5	SYTSWFLDAFNYAIL	92	H5	VSTVQKRELVNPASM
45	D4	SWFLDAFNYAILKKI	93	H4	VQKRELVNPASMQQA
46	D3	LDAFNYAILKKIDVL	94	H3	RELVNPASMQALIA
47	D2	FNYAILKKIDVLNLS	95	H2	VNPASMQALIASAR
48	D1	AILKKIDVLNLSIGG	96	H1	ASMKQALIASARRLP

FIG. 8A

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97	I12	IKDFHVYFRESRDA
98	I11	DAELHIFRVFTNNQV
99	I10	KQALIASARRLPGVN
100	I9	LIASARRLPGVNMFE
101	I8	SARRLPGVNMFEQGH
102	I7	RLPGVNMFEQGHGKL
103	I6	GVNMFEQGHGKLDLL
104	I5	MFEQGHGKLDLLRAY
105	I4	<u>OGHGKLDLLRAYQIL</u>
106	I3	GKLDLLRAYQILNSY
107	I2	DLLRAYQILNSYKPQ
108	I1	RAYQILNSYKPQASL
109	J12	QILNSYKPQASLSPS
110	J11	NSYKPQASLSPSYID
111	J10	KPQASLSPSYIDLTE
112	J9	ASLSPSYIDLTECPY
113	J8	SPSYIDLTECPYMWP
114	J7	YIDLTECPYMWPYCS
115	J6	LTECPYMWPYCSQPI
116	J5	CPYMWPYCSQPIYYG

FIG. 8B